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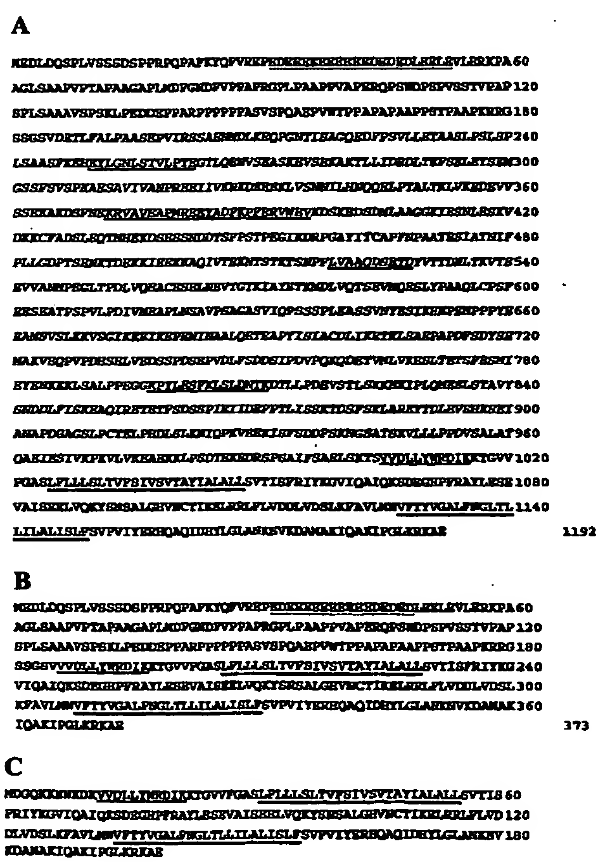

(57) Abstract: NOGO-C polypeptides and polynucleotides and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing NOGO-C polypeptides and polynucleotides in diagnostic assays.

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HUMAN NOGO-C POLYNUCLEOTIDE AND POLYPEPTIDE AND THEIR USES

Field of the Invention

This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in diagnosis and in identifying compounds that may be agonists, antagonists that are potentially useful in therapy, and to production of such polypeptides and polynucleotides.

Background of the Invention

The drug discovery process is currently undergoing a fundamental revolution as it embraces "functional genomics", that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superceding earlier approaches based on "positional cloning". A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

Summary of the Invention

The present invention relates to NOGO-C, in particularNOGO-C polypeptides and NOGO-C polynucleotides, recombinant materials and methods for their production. Such polypeptides and polynucleotides are of interest in relation to methods of treatment of certain diseases, including, but not limited to, neuropathies, spinal injury, brain injury, stroke, neuronal degeneration for example Alzheimer's disease and Parkinson's disease, neuromuscular disorders, psychiatric disorders and developmental disorders, hereinafter referred to as " diseases of the invention". In a further aspect, the invention relates to methods for identifying agonists and antagonists (*e.g.*, inhibitors) using the materials provided by the invention, and treating conditions associated with NOGO-C imbalance with the identified compounds In a still further aspect, the invention relates to diagnostic assays for detecting diseases associated with inappropriateNOGO-C activity or levels.

Description of the Invention

In a first aspect, the present invention relates to NOGO-C polypeptides. Such polypeptides include (a) an isolated polypeptide encoded by a polynucleotide comprising the sequence of SEQ ID NO:1;

(b) an isolated polypeptide encoded by a polynucleotide having the sequence of SEQ ID NO:1;

(c) the polypeptide having the amino acid sequence of SEQ ID NO:2; and

(d) fragments and variants of such polypeptides in (a) to (c).

Polypeptides of the present invention are believed to be members of the reticulon family of polypeptides. They are therefore of interest because members of this family have been shown to display prominent but not exclusive expression in cells of the nervous system. Expression of one isoform of these polypeptides, NSP-C (J. Hens et al. Cell Tissue Res. 292:229-237,1998) has been shown to correlate with neuronal differentiation. Alternative splicing of the genes of this family of polypeptides is known to generate differentially expressed isoforms with overlapping and distinct functions in different tissues (J.G. Geisler et al. Mamm. Genome 9:164-173, 1998). Amino acid similarity between members of this family of polypeptides with fragments of a high-molecular weight protein purified from bovine spinal cord (A.A. Spillmann et al. J. Biol. Chem. 273:15487-15493, 1998) indicates a potential role in axonal growth inhibition role for these proteins. Similarly, expression of NSP-A in specific cancerous cells (N. Senden et al. Histochem. Cell Biol. 108:155-165, 1997) may indicate a potential use of these polypeptides in the diagnosis and or treatment of cancers.

The detection of polynucleotides comprising portions of NOGO in human fetal brain and human adult spinal cord cDNA and an abundant >5kb mRNA isoform in human adult brain together with different transcripts potentially arising by alternative splicing in heart, lung, liver, kidney and skeletal muscle suggests that NOGO isoforms may similarly serve overlapping and distinct functions in these tissues. By analogy with the semaphorin family of neurite-modulatory polypeptides it might be postulated that these different isoforms would function in each of these tissues to control local innervation by distinct neuronal populations. Aberrant expression of specific isoforms within, for example, skeletal muscle would be predicted to alter motor and sensory neuron innervation in diseases such as ALS.

The presence of characteristic signature polypeptides and highly hydrophobic regions in the polypeptide of the present invention suggests that its expression in regions of the nervous system and in tissues forming boundaries for growth may modulate growth and pathfinding both during development and following pathological or injurious processes.

Expression of the polypeptide of the invention, fragments thereof or alternatively spliced variants of the polypeptide on the surface of cells either naturally, as a secreted protein or following release by cellular damage may act on other cells either through specific receptors or pathologically through non-specific interactions to modulate cell attachment, spreading, migration or growth. This inhibition might be expected to be either reversible or permanent possibly resulting in cell death. .

The biological properties of the NOGO-C are hereinafter referred to as "biological activity of NOGO-C" or "NOGO-C activity". Preferably, a polypeptide of the present invention exhibits at least one biological activity of NOGO-C.

Polypeptides of the present invention also includes variants of the aforementioned polypeptides, including all allelic forms and splice variants. Such polypeptides vary from the reference polypeptide by insertions, deletions, and substitutions that may be conservative or non-conservative, or any combination thereof. Particularly preferred variants are those in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acids are inserted, substituted, or deleted, in any combination.

Preferred fragments of polypeptides of the present invention include an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids from the amino acid sequence of SEQ ID NO: 2, or an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids truncated or deleted from the amino acid sequence of SEQ ID NO: 2. Preferred fragments are biologically active fragments that mediate the biological activity of NOGO-C, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also preferred are those fragments that are antigenic or immunogenic in an animal, especially in a human.

Fragments of the polypeptides of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention.The polypeptides of the present invention may be in the form of the "mature" protein or may be a part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence that contains secretory or leader sequences, pro-sequences, sequences that aid in purification, for instance multiple histidine residues, or an additional sequence for stability during recombinant production.

Polypeptides of the present invention can be prepared in any suitable manner, for instance by isolation form naturally occuring sources, from genetically engineered host cells comprising expression systems (*vide infra*) or by chemical synthesis, using for instance automated peptide synthesisers, or a combination of such methods.. Means for preparing such polypeptides are well understood in the art.

In a further aspect, the present invention relates to NOGO-C polynucleotides. Such polynucleotides include:

(a) an isolated polynucleotide encoding the polypeptide of SEQ ID NO:2;

(b) an isolated polynucleotide having the polynucleotide sequence of SEQ ID NO:1; and

polynucleotides that are fragments and variants of the above mentioned polynucleotides or that are complementary to above mentioned polynucleotides, over the entire length thereof.

Preferred fragments of polynucleotides of the present invention include an isolated polynucleotide having at least 15, 30, 50 or 100 contiguous nucleotides from the sequence of SEQ ID NO: 1 or an isolated polynucleotide having at least 30, 50 or 100 contiguous nucleotides truncated or deleted from the sequence of SEQ ID NO: 1.

Preferred variants of polynucleotides of the present invention include splice variants, allelic variants, and polymorphisms, including polynucleotides having one or more single nucleotide polymorphisms (SNPs).

In a further aspect, the present invention provides polynucleotides that are RNA transcripts of the DNA sequences of the present invention. Accordingly, there is provided an RNA polynucleotide encoding the polypeptide of SEQ ID NO:2 and an RNA transcript of the DNA sequence of SEQ ID NO:1 and RNA polynucleotides that are complementary thereto.

The polynucleotide sequence of SEQ ID NO:1 is a splice variant of the human NOGO gene which maps to human chromosome 2p21. Two splice variants of human NOGO have already been disclosed in WO00/05364 (SmithKline Beecham). The polynucleotide sequence of SEQ ID NO:1 is a cDNA sequence that encodes the polypeptide of SEQ ID NO:2. The polynucleotide sequence encoding the polypeptide of SEQ ID NO:2 may be identical to the polypeptide encoding sequence of SEQ ID NO:1 or it may be a sequence other than SEQ ID NO:1, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:2. The polypeptide of the SEQ ID NO:2 is related to other proteins of the reticulon family, having homology and/or structural similarity with Human neuroendocrine-specific protein C (A.J. Roebroek et al., J. Biol. Chem. 268: 13439-13447,1993). The amino acid sequence of SEQ ID NO:2 has been deposited in GenBank with accession number AJ251385.

WO00/05364 (SmithKline Beecham) discloses NOGO-A and NOGO-B splice-variant polynucleotide and polypeptide sequences. SEQ ID NO:3 shows the cDNA sequence of NOGO-A which encodes the polypeptide of SEQ ID NO:4 (deposited in GenBank as AJ251383). SEQ ID NO:5 shows the cDNA sequence of NOGO-B which encodes the polypeotide of SEQ ID NO:6 (deposited in GenBank as AJ251384).

Preferred polypeptides and polynucleotides of the present invention are expected to have, *inter alia*, similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention have at least one NOGO-C activity.

Polynucleotides of the present invention may be obtained using standard cloning and screening techniques from a cDNA library derived from mRNA in cells ofhuman fetal brain and

spinal cord, (see for instance, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself, or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, Proc Natl Acad Sci USA (1989) 86:821-824, or is an HA tag. The polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Polynucleotides that are identical, or have sufficient identity to a polynucleotide sequence of SEQ ID NO:1, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification reaction (for instance, PCR). Such probes and primers may be used to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding paralogs from human sources and orthologs and paralogs from species other than human) that have a high sequence similarity to SEQ ID NO:1, typically at least 95% identity. Preferred probes and primers will generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50, if not at least 100 nucleotides. Particularly preferred probes will have between 30 and 50 nucleotides. Particularly preferred primers will have between 20 and 25 nucleotides.

A polynucleotide encoding a polypeptide of the present invention, including homologs from species other than human, may be obtained by a process comprising the steps of screening a library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO: 1 or a fragment thereof, preferably of at least 15 nucleotides; and isolating full-length cDNA and genomic clones containing said polynucleotide sequence. Such hybridization techniques are well known to the skilled artisan. Preferred stringent hybridization conditions include overnight incubation at 42^{o}C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10 % dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0.1x SSC at about 65^{o}C. Thus the present invention also includes isolated polynucleotides, preferably with a nucleotide sequence of at least 100, obtained by screening a library under

stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO:1 or a fragment thereof, preferably of at least 15 nucleotides.

The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide does not extend all the way through to the 5' terminus. This is a consequence of reverse transcriptase, an enzyme with inherently low "processivity" (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during first strand cDNA synthesis.

There are several methods available and well known to those skilled in the art to obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., Proc Nat Acad Sci USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon (trade mark) technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon (trade mark) technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using 'nested' primers, that is, primers designed to anneal within the amplified product (typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analysed by DNA sequencing and a full-length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems comprising a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression sytems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Polynucleotides may be introduced into host cells by methods described in many standard laboratory manuals, such as Davis et al., Basic Methods in Molecular Biology (1986) and Sambrook *et al.*(*ibid*). Preferred

methods of introducing polynucleotides into host cells include, for instance, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as *Streptococci*, *Staphylococci*, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, episomal and virus-derived systems, *e.g.*, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector that is able to maintain, propagate or express a polynucleotide to produce a polypeptide in a host may be used. The appropriate polynucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, (*ibid*). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and/or purification.

Polynucleotides of the present invention may be used as diagnostic reagents, through detecting mutations in the associated gene. Detection of a mutated form of the gene characterised by the polynucleotide of SEQ ID NO:1 in the cDNA or genomic sequence and which is associated with a dysfunction will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered spatial or temporal expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques well known in the art.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or it may be amplified enzymatically by using PCR, preferably RT-PCR, or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to labeledNOGO-C nucleotide sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence difference may also be detected by alterations in the electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (see, for instance, Myers *et al.*, Science (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (see Cotton *et al.*, Proc Natl Acad Sci USA (1985) 85: 4397-4401).

An array of oligonucleotides probes comprising NOGO-C polynucleotide sequence or fragments thereof can be constructed to conduct efficient screening of *e.g.*, genetic mutations. Such arrays are preferably high density arrays or grids. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability, see, for example, M.Chee et al., Science, 274, 610-613 (1996) and other references cited therein.

Detection of abnormally decreased or increased levels of polypeptide or mRNA expression may also be used for diagnosing or determining susceptibility of a subjectto a disease of the invention. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagonostic kit comprising:

(a) a polynucleotide of the present invention, preferably the nucleotide sequence of SEQ ID NO: 1, or a fragment or an RNA transcript thereof;

(b) a nucleotide sequence complementary to that of (a);

(c) a polypeptide of the present invention, preferably the polypeptide of SEQ ID NO:2 or a fragment thereof; or

(d) an antibody to a polypeptide of the present invention, preferably to the polypeptide of SEQ ID NO:2.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, particularly diseases of the invention, amongst others.

The polynucleotide sequences of the present invention are also valuable tools for tissue expression studies. Such studies allow the determination of expression patterns of polynucleotides of the present invention which may give an indication as to the expression patterns of the encoded polypeptides in tissues, by detecting the mRNAs that encode them. The techniques used are well known in the art and include in situ hydridisation techniques to clones arrayed on a grid, such as cDNA microarray hybridisation (Schena *et al*, Science, 270, 467-470, 1995 and Shalon *et al*, Genome Res, 6, 639-645, 1996) and nucleotide amplification techniques such as PCR. A preferred method uses the TAQMAN (Trade mark) technology available from Perkin Elmer. Results from these studies can provide an indication of the normal function of the polypeptide in the organism. In addition, comparative studies of the normal expression pattern of mRNAs with that of mRNAs encoded by an alternative form of the same gene (for example, one having an alteration in polypeptide coding potential or a regulatory mutation) can provide valuable insights into the role of the polypeptides of the present invention, or that of inappropriate expression thereof in disease. Such inappropriate expression may be of a temporal, spatial or simply quantitative nature.

The polypeptides of the present invention are expressed in brain, heart, liver, skeletal muscle, pancreas and kidney; based on Northern blot data provided in figure 1.

A further aspect of the present invention relates to antibodies. The polypeptides of the invention or their fragments, or cells expressing them, can be used as immunogens to produce antibodies that are immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique

which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., Nature (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, Immunology Today (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, 77-96, Alan R. Liss, Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography. Antibodies against polypeptides of the present invention may also be employed to treat diseases of the invention, amongst others.

Polypeptides and polynucleotides of the present invention may also be used as vaccines. Accordingly, in a further aspect, the present invention relates to a method for inducing an immunological response in a mammal that comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said animal from disease, whether that disease is already established within the individual or not. An immunological response in a mammal may also be induced by a method comprises delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce such an immunological response to produce antibody to protect said animal from diseases of the invention. One way of administering the vector is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid. For use a vaccine, a polypeptide or a nucleic acid vector will be normally provided as a vaccine formulation (composition). The formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous, intramuscular, intravenous, or intradermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions that may contain anti-oxidants, buffers, bacteriostats and solutes that render the formulation instonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions that may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The

vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Polypeptides of the present invention have one or more biological functions that are of relevance in one or more disease states, in particular the diseases of the invention hereinbefore mentioned. It is therefore useful to to identify compounds that stimulate or inhibit the function or level of the polypeptide. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those that stimulate or inhibit the function or level of the polypeptide. Such methods identify agonists or antagonists that may be employed for therapeutic and prophylactic purposes for such diseases of the invention as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, collections of chemical compounds, and natural product mixtures. Such agonists or antagonists so-identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; a structural or functional mimetic thereof (see Coligan*et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)) or a small molecule.

The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof, by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve measuring or detecting (qualitatively or quantitatively) the competitive binding of a candidate compound to the polypeptide against a labeled competitor (*e.g.* agonist or antagonist). Further, these screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring a NOGO-C activity in the mixture, and comparing the NOGO-C activity of the mixture to a control mixture which contains no candidate compound.

Polypeptides of the present invention may be employed in conventional low capacity screening methods and also in high-throughput screening (HTS) formats. Such HTS formats include not only the well-established use of 96- and, more recently, 384-well micotiter plates but also emerging methods such as the nanowell method described by Schullek et al, Anal Biochem., 246, 20-29, (1997).

Fusion proteins, such as those made from Fc portion and NOGO-C polypeptide, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, J Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, J Biol Chem, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the polypeptide of the present invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptideusing monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents that may inhibit or enhance the production of polypeptide(also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

A polypeptide of the present invention may be used to identify membrane bound or soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance, ^{125}I), chemically modified (for instance, biotinylated), or fused to a peptide sequence suitable for detection or purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supernatants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide that compete with the binding of the polypeptideto its receptors, if any. Standard methods for conducting such assays are well understood in the art.

Examples of antagonists of polypeptides of the present invention include antibodies or, in some cases, oligonucleotides or proteins that are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, *e.g.*, a fragment of the ligands, substrates, receptors, enzymes, etc.; or a small molecule that bind to the polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Screening methods may also involve the use of transgenic technology and NOGO-C gene. The art of constructing transgenic animals is well established. For example, the NOGO-C gene may be introduced through microinjection into the male pronucleus of fertilized oocytes, retroviral transfer into pre- or post-implantation embryos, or injection of genetically modified, such as by electroporation, embryonic stem cells into host blastocysts. Particularly useful transgenic animals are so-called "knock-in" animals in which an animal gene is replaced by the human equivalent within the genome of that animal. Knock-in transgenic animals are useful in the drug discovery process, for target validation, where the compound is specific for the human target. Other useful transgenic animals are so-called "knock-out" animals in which the expression of the animal ortholog of a polypeptide of the present invention and encoded by an endogenous

DNA sequence in a cell is partially or completely annulled. The gene knock-out may be targeted to specific cells or tissues, may occur only in certain cells or tissues as a consequence of the limitations of the technology, or may occur in all, or substantially all, cells in the animal. Transgenic animal technology also offers a whole animal expression-cloning system in which introduced genes are expressed to give large amounts of polypeptides of the present invention

Screening kits for use in the above described methods form a further aspect of the present invention. Such screening kits comprise:

(a) a polypeptide of the present invention;

(b) a recombinant cell expressing a polypeptide of the present invention;

(c) a cell membrane expressing a polypeptide of the present invention; or

(d) an antibody to a polypeptide of the present invention;

which polypeptide is preferably that of SEQ ID NO:2.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

Glossary

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

"Antibodies" as used herein includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, including the products of an Fab or other immunoglobulin expression library.

"Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is "isolated" even if it is still present in said organism, which organism may be living or non-living.

"Polynucleotide" generally refers to any polyribonucleotide (RNA) or polydeoxribonucleotide (DNA), which may be unmodified or modified RNA or DNA. "Polynucleotides" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-stranded regions

comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any polypeptide comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, Proteins - Structure and Molecular Properties, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., Post-translational Protein Modifications: Perspectives and Prospects, 1-12, in Post-translational Covalent Modification of Proteins, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and

nonprotein cofactors", Meth Enzymol, 182, 626-646, 1990, and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", Ann NY Acad Sci, 663, 48-62, 1992).

"Fragment" of a polypeptide sequence refers to a polypeptide sequence that is shorter than the reference sequence but that retains essentially the same biological function or activity as the reference polypeptide. "Fragment" of a polynucleotide sequence refers to a polynucloetide sequence that is shorter than the reference sequence of SEQ ID NO:1.

"Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains the essential properties thereof. A typical variant of a polynucleotide differs in nucleotide sequence from the reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from the reference polypeptide. Generally, alterations are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, insertions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. Typical conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe and Tyr. A variant of a polynucleotide or polypeptide may be naturally occurring such as an allele, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis. Also included as variants are polypeptides having one or more post-translational modifications, for instance glycosylation, phosphorylation, methylation, ADP ribosylation and the like. Embodiments include methylation of the N-terminal amino acid, phosphorylations of serines and threonines and modification of C-terminal glycines.

"Allele" refers to one of two or more alternative forms of a gene occuring at a given locus in the genome.

"Polymorphism" refers to a variation in nucleotide sequence (and encoded polypeptide sequence, if relevant) at a given position in the genome within a population.

"Single Nucleotide Polymorphism" (SNP) refers to the occurence of nucleotide variability at a single nucleotide position in the genome, within a population. An SNP may occur within a gene or within intergenic regions of the genome. SNPs can be assayed using Allele Specific Amplification (ASA). For the process at least 3 primers are required. A common primer is used in reverse complement to the polymorphism being assayed. This common primer can be between 50 and 1500 bps from the polymorphic base. The other two (or more) primers are

identical to each other except that the final 3' base wobbles to match one of the two (or more) alleles that make up the polymorphism. Two (or more) PCR reactions are then conducted on sample DNA, each using the common primer and one of the Allele Specific Primers.

"Splice Variant" as used herein refers to cDNA molecules produced from RNA molecules initially transcribed from the same genomic DNA sequence but which have undergone alternative RNA splicing. Alternative RNA splicing occurs when a primary RNA transcript undergoes splicing, generally for the removal of introns, which results in the production of more than one mRNA molecule each of that may encode different amino acid sequences. The term splice variant also refers to the proteins encoded by the above cDNA molecules.

"Identity" reflects a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, determined by comparing the sequences. In general, identity refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of the two polynucleotide or two polypeptide sequences, respectively, over the length of the sequences being compared.

"% Identity" - For sequences where there is not an exact correspondence, a "% identity" may be determined. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in either one or both sequences, to enhance the degree of alignment. A % identity may be determined over the whole length of each of the sequences being compared (so-called global alignment), that is particularly suitable for sequences of the same or very similar length, or over shorter, defined lengths (so-called local alignment), that is more suitable for sequences of unequal length.

"Similarity" is a further, more sophisticated measure of the relationship between two polypeptide sequences. In general, "similarity" means a comparison between the amino acids of two polypeptide chains, on a residue by residue basis, taking into account not only exact correspondences between a between pairs of residues, one from each of the sequences being compared (as for identity) but also, where there is not an exact correspondence, whether, on an evolutionary basis, one residue is a likely substitute for the other. This likelihood has an associated "score" from which the "% similarity" of the two sequences can then be determined.

Methods for comparing the identity and similarity of two or more sequences are well known in the art. Thus for instance, programs available in the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J et al, Nucleic Acids Res, 12, 387-395, 1984, available from Genetics Computer Group, Madison, Wisconsin, USA), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % similarity between two polypeptide sequences. BESTFIT uses the "local homology" algorithm of Smith and Waterman (J Mol Biol, 147,195-197, 1981, Advances in Applied Mathematics, 2, 482-489, 1981) and finds the best single region of similarity between two

sequences. BESTFIT is more suited to comparing two polynucleotide or two polypeptide sequences that are dissimilar in length, the program assuming that the shorter sequence represents a portion of the longer. In comparison, GAP aligns two sequences, finding a "maximum similarity", according to the algorithm of Neddleman and Wunsch (J Mol Biol, 48, 443-453, 1970). GAP is more suited to comparing sequences that are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters "Gap Weight" and "Length Weight" used in each program are 50 and 3, for polynucleotide sequences and 12 and 4 for polypeptide sequences, respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned.

Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, J Mol Biol, 215, 403-410, 1990, Altschul S F et al, Nucleic Acids Res., 25:389-3402, 1997, available from the National Center for Biotechnology Information (NCBI), Bethesda, Maryland, USA and accessible through the home page of the NCBI at www.ncbi.nlm.nih.gov) and FASTA (Pearson W R, Methods in Enzymology, 183, 63-99, 1990; Pearson W R and Lipman D J, Proc Nat Acad Sci USA, 85, 2444-2448,1988, available as part of the Wisconsin Sequence Analysis Package).

Preferably, the BLOSUM62 amino acid substitution matrix (Henikoff S and Henikoff J G, Proc. Nat. Acad Sci. USA, 89, 10915-10919, 1992) is used in polypeptide sequence comparisons including where nucleotide sequences are first translated into amino acid sequences before comparison.

Preferably, the program BESTFIT is used to determine the % identity of a query polynucleotide or a polypeptide sequence with respect to a reference polynucleotide or a polypeptide sequence, the query and the reference sequence being optimally aligned and the parameters of the program set at the default value, as hereinbefore described.

"Identity Index" is a measure of sequence relatedness which may be used to compare a candidate sequence (polynucleotide or polypeptide) and a reference sequence. Thus, for instance, a candidate polynucleotide sequence having, for example, an Identity Index of 0.95 compared to a reference polynucleotide sequence is identical to the reference sequence except that the candidate polynucleotide sequence may include on average up to five differences per each 100 nucleotides of the reference sequence. Such differences are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion. These differences may occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between these terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to obtain a polynucleotide sequence having an Identity Index of 0.95 compared to a reference polynucleotide sequence, an average of up to 5 in every 100 of the

nucleotides of the in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

Similarly, for a polypeptide, a candidate polypeptide sequence having, for example, an Identity Index of 0.95 compared to a reference polypeptide sequence is identical to the reference sequence except that the polypeptide sequence may include an average of up to five differences per each 100 amino acids of the reference sequence. Such differences are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion. These differences may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between these terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to obtain a polypeptide sequence having an Identity Index of 0.95 compared to a reference polypeptide sequence, an average of up to 5 in every 100 of the amino acids in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

The relationship between the number of nucleotide or amino acid differences and the Identity Index may be expressed in the following equation:

$$\mathbf{n_a} \leq \mathbf{x_a} - (\mathbf{x_a} \bullet \mathbf{I}),$$

in which:

$\mathbf{n_a}$ is the number of nucleotide or amino acid differences,

$\mathbf{x_a}$ is the total number of nucleotides or amino acids in SEQ ID NO:1 or SEQ ID NO:2, respectively,

I is the Identity Index ,

• is the symbol for the multiplication operator, and

in which any non-integer product of $\mathbf{x_a}$ and **I** is rounded down to the nearest integer prior to subtracting it from $\mathbf{x_a}$.

"Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a reference sequence. Such relatedness may be quantified by determining the degree of identity and/or similarity between the two sequences as hereinbefore defined. Falling within this generic term are the terms "ortholog", and "paralog". "Ortholog" refers to a polynucleotide or polypeptide that is the functional equivalent of the polynucleotide or polypeptide in another species. "Paralog" refers to a polynucleotideor polypeptide that within the same species which is functionally similar.

"Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 *** discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, *e.g.*, EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified.

All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be incorporated by reference herein as being fully set forth. Any patent application to which this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

Examples

Example 1 – Cloning of NOGO cDNAs

Primers designed against ESTs containing peptides reported for a bovine IN-1 reactive inhibitory protein (Spillmann, A.A., et al (1998) *J Biol Chem.* 273, 19283-19293) were used in standard PCR amplifications from human fetal brain or human spinal cord cDNA (Clontech). These products were cloned into pGEMTeasy (Promega), sequenced and this data used to search for new ESTs extending the known sequence until multiple sequences containing in-frame upstream stop codons were identified. IMAGE clones (NOGO-B IMAGE 590987, NOGO-C IMAGE 561867) were obtained from Research Genetics, and fully sequenced on both strands. The full ORF for NOGO-A was amplified from human spinal cord cDNA (Clontech) using the sense primer (GTGCTCGAGC CAGCCATGGAAGACCTGGACCAGTCTCCTCTGG) and the antisense primer (GAATCTAGACTAATTATTTTGGGCGTTTTCATTCAGCTTTGC). Epitope tagged versions of NOGO-A cDNA were made in pcDNA3 (Invitrogen) using standard PCR techniques (N terminal FLAG tag or C terminal myc tag).

Example 2 - Tissue distribution of NOGO

A radioactively labelled DNA probe corresponding to the C-terminal 2kb of the NOGO open reading frame was hybridised with a Clontech MTN-1 filter containing equivalent loadings of mRNA from each of the indicated tissues and then washed to high stringency to only detect NOGO transcripts. At least three bands are visible (>5kb, 2.4kb and <2kb). The NOGO-A transcript is present in adult brain and to a lesser degree in heart and skeletal muscle. The NOGO-B transcript is present at essentially similar levels in all tissues while the NOGO-C transcript is more specifically expressed, most abundantly in skeletal muscle, brain and kidney with low levels detectable in the pancreas.

Example 3 – Demonstration of neurite inhibitory activity

In order to assess whether NOGO possessed neurite inhibitory activity a soluble version of the 220 kD isoform (NOGO-A) was prepared. The extracellular region of the 220 kD protein was prepared as a bivalent Fc chimeric protein using a CD33 signal-sequence and human IgG-Fc sequences and the purified protein was placed in model systems to assess neurite inhibitory activity.

Fc Preparation

The entire putative extracellular domain (ECD) of NOGO-A (residues 1-1024) was amplified by PCR and cloned into signal pIg-plus (R&D Systems) between the CD33 signal sequence and

human IgG sequence using engineered XhoI-XbaI sites to produce a secreted chimeric fusion protein with a carboxy terminal Fc portion. NOGO fusion protein was purified from COS-7 conditioned medium, following DEAE-Dextran transfections, using protein A sepharose (Sigma). Dissociated cerebellar granule neurons (CGC) were allowed to adhere to substrate and then treated with control Fc protein (SIRP-Fc), MAG-Fc, or NOGO-Fc. The control protein SIRP-Fc had no effect on neurite-outgrowth while the inhibitory effects of MAG and NOGO were dose dependent and were equally potent in this model. This experiment shows that recombinant soluble NOGO produced as a bivalent Fc is a potent neurite outgrowth inhibitory molecule comparable to MAG.

Example 4 – Purified GST-NOGO fusion proteins inhibit hippocampal neurite outgrowth

This example investigated the effect of purified GST-NOGO fusion proteins (GST: glutathione-S-transferase) on cultured hippocampal neurite outgrowth. The fusion proteins created for examples 4 and 5 consist of:

i) GST alone;

ii) GST-Nogo "splice" encoding Nogo-A amino acids 185-1004 (which represent the entire splice region specific to Nogo-A); and

iii) GST-Nogo "loop" encoding amino acids 1055-1120 (representing the intertransmembrane loop present in all Nogo isoforms).

Cultured E18 embryonic hippocampal neurons in polylysine coated 96 well plates at a density of 20,000 cells per well in Eagle's basal medium supplemented to contain 25mM KCl, 10% FCS and 50ug/ml gentamycin were supplemented with purified fusion proteins in triplicate wells then incubated for 48 hours. Cells were fixed with 4% paraformaldehyde then stained using coomassie blue. Neurite length was determined using a KS300 Image analysis system. Results are expressed as a percentage of the length of neurites of cells treated with PBS alone and are shown in Table 1.

Both NOGO fusion proteins clearly inhibit hippocampal neurite-outgrowth confirming the presence of two independent neurite inhibitory domains, one present in the NOGO-A specific splice region and one in the NOGO-A, B and C common intertransmembrane loop region.

Table 1.

Treatment	Neurite Length (% of untreated control)
GST 20nM	93 ± 5.1
GST 160nM	95 ± 9
GST-Nogo loop 1nM	78 ± 3.6

GST-Nogo loop 20nM	60 ± 2.3
GST-Nogo loop 160nM	66 ± 1.8
GST-Nogo splice 1nM	98 ± 3.1
GST-Nogo splice 20nM	95 ± 3.8
GST-Nogo splice 160nM	62 ± 3.9

Example 5 - Purified GST-NOGO fusion proteins inhibit differentiated PC12 neurite outgrowth

NGF differentiated PC12 cells were cultured in 96 well plates and treated with purified GST and GST-Nogo fusion proteins (described in example 4) at the indicated concentrations, incubated for a further 72hours, fixed and stained with coomassie blue. Neurite-length was determined using a KS300 Image analysis system. Results are expressed as the length of neurites in μm and are shown in Table 2.

GST-NOGO loop and GST-NOGO splice both significantly affect neurite outgrowth from PC12 cells at the concentrations tested. Both Nogo fusion proteins clearly inhibit PC12 neurite-outgrowth confirming the presence of two independent neurite inhibitory domains, one present in the NOGO-A specific splice region and one in the NOGO-A, B and C common intertransmembrane loop region.

Table 2.

Treatment	Mean Neurite-length (μm)	Standard deviation
No Protein	32.09	
GST 6μM	27.95	2.31
GSTNogoLoop 2.6μM	24.7	3.43
GSTNogoloop 8μM	20.59	1.99
GSTNogo splice 3.8μM	29.49	5.25
GSTNogo splice 6.4μM	20.2	4.65

Example 6 – Nogo expression in pMCAO rat model of stroke

TAQMAN ™ analysis of cDNA preparations made from samples of tissues taken from either the ipsilateral or contralateral side of permanent MCAO treated rats was performed to analayse changes in NOGO-A expression following the ischaemic insult. The results are shown in Fig 3.

NOGO-A expression was significantly increased in the MCAO treated samples within three hours and remained high to the end of the trial period at 24 hours. Similar changes were not observed in samples from the contralateral side or in sham operated animal samples.

These data suggest very strongly that increases in NOGO-A expression correlate with the onset of ischaemic damage and may be a causative factor.

Antagonists of NOGO-A activity could therefore be expected to protect from ischaemic damage as occurs in stroke patients.

In the figures:

Figure 1 depicts a Northern blot showing tissue distribution of human NOGO. Where lane 1 contains human adult heart RNA, lane 2 contains human adult brain RNA, lane 3 contains human placental RNA, lane 4 contains human adult lung RNA, lane 5 contains human adult liver RNA , lane 6 contains human adult skeletal muscle RNA, lane 7 contains human adult kidney RNA and lane 8 contains human adult pancreas RNA.

Figure 2 Amino acids matching all six published peptide sequences from purified bNI-220 are shown with a thick underline. The location of putative transmembrane domains is shown double underlined. An acid box motif is marked with a dotted underline. Amino acids absent in the shorter splice variants of NOGO are shown in italics (residues 186-1004).

A. Predicted amino acid sequence of NOGO-A (GenBank Accession number AJ251383).

B. Predicted amino acid sequence of NOGO-B (GenBank Accession number AJ251384).

C. Predicted amino acid sequence of NOGO-C (GenBank Accession number AJ251385).

Figure 3. Nogo-A expression levels in pMCAO rat stroke model. NOGO-A levels are shown as % GAPDH (a standard housekeeping gene). The data is shown for ipsilateral (L) and contralateral (R) in naïve animals and at post-operative time points of 3 hours, 6 hours, 12 hours and 24 hours. Data is also shown for sham operated (white bars) animals.

SEQUENCE INFORMATION

SEQ ID NO:1

ATGGACGGTCAGAAGAAAAATTGGAAGGACAAGGTTGTTGACCTCCTGTACTGGAGAGAC
ATTAAGAAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTA
TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC
TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC
AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT
TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT
GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC
TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT
ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT
AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA

SEQ ID NO:2

MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS
FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVD
DLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNV
KDAMAKIQAKIPGLKRKAE

SEQ ID NO:3

ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACCCCGGCCGCAG
CCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAAGAGGAGGAG
GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGCCCGCC
GCCGGGCTGTCCGCGGCCCCAGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTGATGGAC
TTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCCGTC
GCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCCGCGCCA
TCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAGCCTCCG
GCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTGTGGACC
CCGCCAGCCCCGGCTCCCGCCGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGCAGGGGC
TCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCTGTGATA
CGCTCCTCTGCAGAAAATATGGACTTGAAGGAGCAGCCAGGTAACACTATTTCGGCTGGT
CAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCTCTGTCTCCT
CTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCC
ACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAAGGCA
AAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATG
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TCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATG
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GAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTGGAAAGTAAAGTG
GATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAAGATAGTGAGAGT
AGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGATCGTCCAGGAGCA

TATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCAACAAACATTTTT
CCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAAATAGAAGAAAAG
AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCCTTTTCTTGTA
GCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACAAAGGTGACTGAG
GAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTGAA
AGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAAATGGACTTGGTT
CAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCATTT
GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAAGCACCATTG
AATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTAGAA
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GAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAGCCATATTTG
GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGATGAAGTTTCA
ACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTTAT
TCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAAACGTTTTCA
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TCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT
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Claims

1. An isolated polypeptide encoded by a polynucleotide comprising the sequence of SEQ ID NO:1.

2. An isolated polypeptide according to claim 1 encoded by a polynucleotide having the sequence of SEQ ID NO:1.

3. An isolated polypeptide according to claim 1 or 2 having the amino acid sequence of SEQ ID NO:2.

4. An isolated polypeptide which is a fragment or variant of an isolated polypeptideof any one of claims 1 to 3.

5. An isolated polynucleotide selected from the group consisting of:
(a) an isolated polynucleotide encoding the polypeptide of SEQ ID NO:2;
(b) an isolated polynucleotide having the polynucleotide sequence of SEQ ID NO:1;and
(c) an isolated polynucleotide that is a fragment or variant of the polynucleotides of (a) or (b); or polynucleotides that are complementary to such polynucleotides, over the entire length thereof.

6. An expression system comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression vector is present in a compatible host cell.

7. A recombinant host cell comprising the expression vector of claim 6 or a membrane thereof expressing the polypeptide of claim 1.

8. A process for producing a polypeptide of claim 1 comprising the step of culturing a host cell as defined in claim 7 under conditions sufficient for the production of said polypeptide and recovering the polypeptide from the culture medium.

9. An antibody immunospecific for the polypeptide of any one of claims 1 to 3.

10. A method for screening to identify compounds that stimulate or inhibit the function or level of the polypeptide of claim 1 comprising a method selected from the group consisting of:
(a) measuring or, detecting, quantitatively or qualitatively, the bindingof a candidate compound to the polypeptide (or to the cells or membranes expressing the polypeptide) or a fusion protein thereof by means of a label directly or indirectly associated with the candidate compound;

(b) measuring the competition of binding of a candidate compound to the polypeptide (or to the cells or membranes expressing the polypeptide) or a fusion protein thereof in the presence of a labeled competitior;

(c) testing whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells or cell membranes expressing the polypeptide;

(d) mixing a candidate compound with a solution containing a polypeptide of claim 1, to form a mixture, measuring activity of the polypeptide in the mixture, and comparing the activity of the mixture to a control mixture which contains no candidate compound; or

(e) detecting the effect of a candidate compound on the production of mRNA encoding said polypeptide or said polypeptide in cells, using for instance, an ELISA assay.

Figure 1

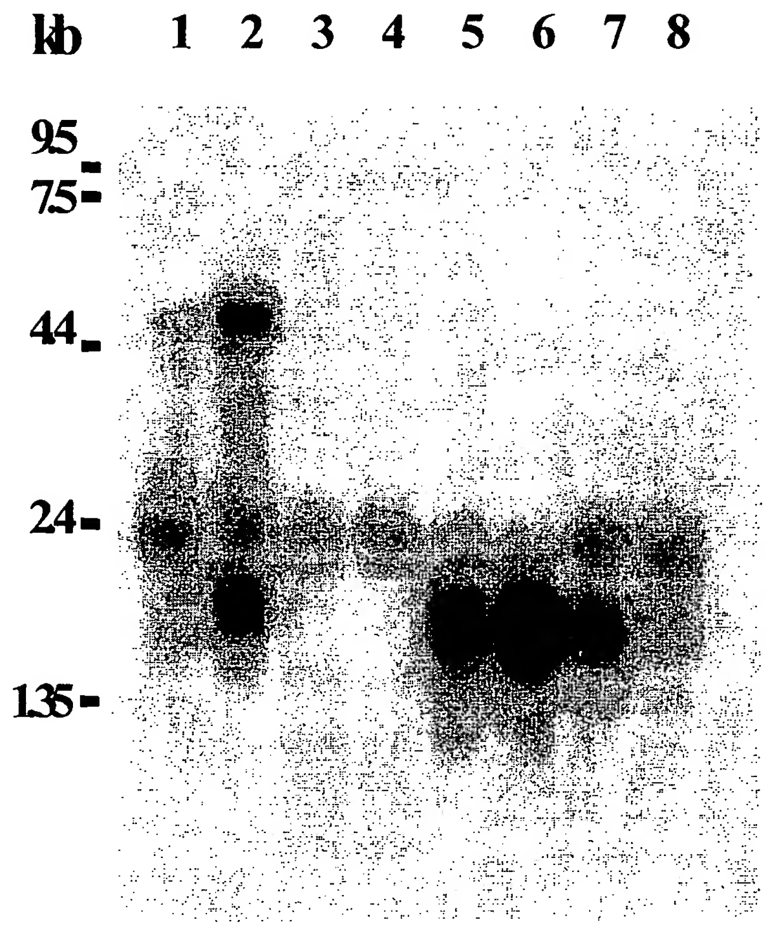

Figure 2

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Figure 2 (continued)

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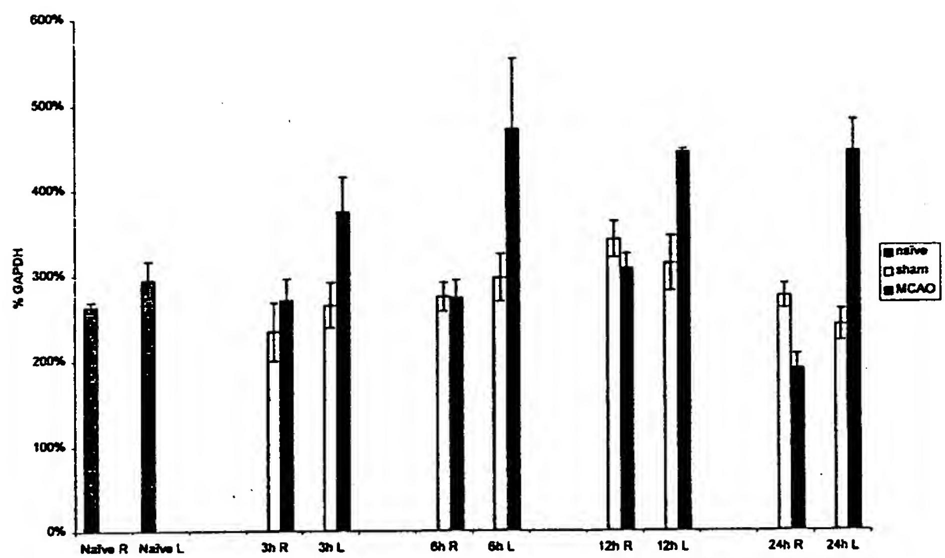
Figure 3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930 935 940

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340 345 350

Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
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INTERNATIONAL SEARCH REPORT

Intern ıal Application No
PCT/GB 00/04345

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C07K14/47 C07K16/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, STRAND

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 06841 A (INCYTE PHARMACEUTICALS, INC.) 19 February 1998 (1998-02-19) abstract page 1, line 1 -page 2, line 41 page 5, line 7 -page 28, line 8 SEQ ID NOS: 1 and 2 page 38 -page 39 page 46; claims 1-14 ---	1-10

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 March 2001	30/03/2001

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Fuchs, U

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 56804 A (HUMAN GENOME SCIENCES, INC.) 17 December 1998 (1998-12-17) abstract page 2, line 1 - line 8 gene no.: 69 page 62, line 1 - line 32 page 82; table 1 page 85, line 1 -page 105, line 7 page 111, line 6 -page 112, line 16 page 113, line 1 -page 120, line 8 SEQ ID NO: 79 page 235 -page 236 SEQ ID NO: 301 page 354 -page 355 page 370 -page 373; claims 1-23 ---	1-10
X	EMBL database, Heidelberg, FRG Emhuml accession number AF077050 27 April 1999 SONG, H. ET AL.: "Homo sapiens neuroendocrine-specific protein C homolog mRNA, complete cds." XP002162897 the whole document	1-8
X	-& EMBL database, Heidelberg, FRG Trembl accession number Q9Y293 1 November 1999 SONG, H. ET AL.: "Human neuroendocrine-specific protein C (NSP) homolg gene." XP002162898 the whole document ---	1-8
A	SPILLMANN, A.A. ET AL: "Identification and Characterization of a Bovine Neurite Growth Inhibitor (bNI-220)" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 30, 24 July 1998 (1998-07-24), pages 19283-19293, XP002162896 cited in the application see especially * page 19288, line 40 - line 56 * * page 19290; table 2 * the whole document ---	1-10

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/GB 00/04345

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ROEBROEK, A.J. ET AL.: "Cloning and Expression of Alternative Transcripts of a Novel Neuroendocrine-specific Gene and Identification of Its 135-kDa Translational Product" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 268, no. 18, 25 June 1993 (1993-06-25), pages 13439-13447, XP002045108 cited in the application the whole document ---	1-10
P,X	PRINJHA, R. ET AL.: "Inhibitor of neurite outgrowth in humans" NATURE, vol. 403, no. 6768, 27 January 2000 (2000-01-27), pages 383-384, XP002144397 the whole document	1-8
P,X	-& EMBL database, Heidelberg, FRG Emhum4 accession number AJ251385 22 July 2000 MICHALOVICH, D.: "Homo sapiens mRNA for Nogo-C protein (Nogo gene)" XP002162899 the whole document -----	1-8

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INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/GB 00/04345

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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		EP 0988385 A	29-03-2000
		US 6046031 A	04-04-2000
		WO 9831818 A	23-07-1998
		AU 8474398 A	08-02-1999
		EP 1000084 A	17-05-2000
		WO 9902546 A	21-01-1999